RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: _10/532,014_

Source: _PCT_

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PCT

RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/532,014

DATE: 02/22/2006
TIME: 08:26:00

Input Set : **A:\Sequence-List.txt**
Output Set: **N:\CRF4\02222006\J532014.raw**

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       3 <110> APPLICANT: Karolinska Innovations AB
       4       Ingelman-Sundberg, Magnus
       5       Karlgren, Maria
       6       Gomez, Alvin
       8 <120> TITLE OF INVENTION: Drug target in cancer therapy
      10 <130> FILE REFERENCE: P05980PC00/HAM/em
C-->  12 <140> CURRENT APPLICATION NUMBER: US/10/532,014
C-->  12 <141> CURRENT FILING DATE: 2005-04-20
      12 <150> PRIOR APPLICATION NUMBER: SE0203137-5
      13 <151> PRIOR FILING DATE: 2002-10-24
      15 <150> PRIOR APPLICATION NUMBER: US 60/420,787
      16 <151> PRIOR FILING DATE: 2002-10-24
      18 <160> NUMBER OF SEQ ID NOS: 10
      20 <170> SOFTWARE: PatentIn version 3.1
      22 <210> SEQ ID NO: 1
      23 <211> LENGTH: 27
      24 <212> TYPE: DNA
      25 <213> ORGANISM: Homo sapiens
      27 <220> FEATURE:
W-->  28 <221> NAME/KEY: Primer
      29 <222> LOCATION: (1)..(27)
      30 <223> OTHER INFORMATION:
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      34 gaggtggagg catcttcttc tcatctg                                     27
      37 <210> SEQ ID NO: 2
      38 <211> LENGTH: 25
      39 <212> TYPE: DNA
      40 <213> ORGANISM: Homo sapiens
      42 <220> FEATURE:
W-->  43 <221> NAME/KEY: primer
      44 <222> LOCATION: (1)..(25)
      45 <223> OTHER INFORMATION:
W-->  48 <400> 2
      49 ctggatcagg gcgtccacat agctg                                       25
      52 <210> SEQ ID NO: 3
      53 <211> LENGTH: 23
      54 <212> TYPE: DNA
      55 <213> ORGANISM: homo sapiens
      57 <220> FEATURE:
W-->  58 <221> NAME/KEY: primer
      59 <222> LOCATION: (1)..(23)
      60 <223> OTHER INFORMATION:
W-->  63 <400> 3
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PATENT APPLICATION: US/10/532,014   TIME: 08:26:00

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        64 agctatgtgg acgccctgat cca                              23
        67 <210> SEQ ID NO: 4
        68 <211> LENGTH: 23
        69 <212> TYPE: DNA
        70 <213> ORGANISM: homo sapiens
        72 <220> FEATURE:
W-->    73 <221> NAME/KEY: primer
        74 <222> LOCATION: (1)..(23)
        75 <223> OTHER INFORMATION:
W-->    78 <400> 4
        79 acgcggtcta gctcctcctg cac                              23
        82 <210> SEQ ID NO: 5
        83 <211> LENGTH: 15
        84 <212> TYPE: PRT
        85 <213> ORGANISM: homo sapiens
        87 <220> FEATURE:
        88 <221> NAME/KEY: peptide
        89 <222> LOCATION: (1)..(15)
        90 <223> OTHER INFORMATION:
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        95 Thr Met Arg Pro Arg Ala Gln Ala Leu Cys Ala Val Pro Arg Pro
        96 1               5                   10                  15
        99 <210> SEQ ID NO: 6
       100 <211> LENGTH: 27
       101 <212> TYPE: DNA
       102 <213> ORGANISM: homo sapiens
       104 <220> FEATURE:
W-->   105 <221> NAME/KEY: primer
       106 <222> LOCATION: (1)..(27)
       107 <223> OTHER INFORMATION:
W-->   110 <400> 6
       111 gacagatcta tggccctgct gctcttg                          27
       114 <210> SEQ ID NO: 7
       115 <211> LENGTH: 28
       116 <212> TYPE: DNA
       117 <213> ORGANISM: homo sapiens
       119 <220> FEATURE:
W-->   120 <221> NAME/KEY: primer
       121 <222> LOCATION: (1)..(28)
       122 <223> OTHER INFORMATION:
W-->   125 <400> 7
       126 gactctagac tagggcctgg gcaccgca                         28
       129 <210> SEQ ID NO: 8
       130 <211> LENGTH: 490
       131 <212> TYPE: PRT
       132 <213> ORGANISM: homo sapiens
       134 <400> SEQUENCE: 8
       136 Met Ala Leu Leu Leu Leu Leu Phe Leu Gly Leu Leu Gly Leu Trp Gly
       137 1               5                   10                  15
```

```
140 Leu Leu Cys Ala Cys Ala Gln Asp Pro Ser Pro Ala Ala Arg Trp Pro
141         20              25              30
144 Pro Gly Pro Arg Pro Leu Pro Leu Val Gly Asn Leu His Leu Leu Arg
145         35              40              45
148 Leu Ser Gln Gln Asp Arg Ser Leu Met Glu Leu Ser Glu Arg Tyr Gly
149     50              55              60
152 Pro Val Phe Thr Val His Leu Gly Arg Gln Lys Thr Val Val Leu Thr
153 65              70              75              80
156 Gly Phe Glu Ala Val Lys Glu Ala Leu Ala Gly Pro Gly Gln Glu Leu
157             85              90              95
160 Ala Asp Arg Pro Pro Ile Ala Ile Phe Gln Leu Ile Gln Arg Gly Gly
161             100             105             110
164 Gly Ile Phe Phe Ser Ser Gly Ala Arg Trp Arg Ala Ala Arg Gln Phe
165         115             120             125
168 Thr Val Arg Ala Leu His Ser Leu Gly Val Gly Arg Glu Pro Val Ala
169         130             135             140
172 Asp Lys Ile Leu Gln Glu Leu Lys Cys Leu Ser Gly Gln Leu Asp Gly
173 145             150             155             160
176 Tyr Arg Gly Arg Pro Phe Pro Leu Ala Leu Leu Gly Trp Ala Pro Ser
177             165             170             175
180 Asn Ile Thr Phe Ala Leu Leu Phe Gly Arg Arg Phe Asp Tyr Arg Asp
181         180             185             190
184 Pro Val Phe Val Ser Leu Leu Gly Leu Ile Asp Glu Val Met Val Leu
185         195             200             205
188 Leu Gly Ser Pro Gly Leu Gln Leu Phe Asn Val Tyr Pro Trp Leu Gly
189     210             215             220
192 Ala Leu Leu Gln Leu His Arg Pro Val Leu Arg Lys Ile Glu Glu Val
193 225             230             235             240
196 Arg Ala Ile Leu Arg Thr Leu Leu Glu Ala Arg Arg Pro His Val Cys
197             245             250             255
200 Pro Gly Asp Pro Val Cys Ser Tyr Val Asp Ala Leu Ile Gln Gln Gly
201             260             265             270
204 Gln Gly Asp Asp Pro Glu Gly Leu Phe Ala Glu Ala Asn Ala Val Ala
205         275             280             285
208 Cys Thr Leu Asp Met Val Met Ala Gly Thr Glu Thr Thr Ser Ala Thr
209     290             295             300
212 Leu Gln Trp Ala Ala Leu Leu Met Gly Arg His Pro Asp Val Gln Gly
213 305             310             315             320
216 Arg Val Gln Glu Glu Leu Asp Arg Val Leu Gly Pro Gly Arg Thr Pro
217             325             330             335
220 Arg Leu Glu Asp Gln Gln Ala Leu Pro Tyr Thr Ser Ala Val Leu His
221             340             345             350
224 Glu Val Gln Arg Phe Ile Thr Leu Leu Pro His Val Pro Arg Cys Thr
225         355             360             365
228 Ala Ala Asp Thr Gln Leu Gly Gly Phe Leu Leu Pro Lys Gly Thr Pro
229     370             375             380
232 Val Ile Pro Leu Leu Thr Ser Val Leu Leu Asp Glu Thr Gln Trp Gln
233 385             390             395             400
236 Thr Pro Gly Gln Phe Asn Pro Gly His Phe Leu Asp Ala Asn Gly His
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RAW SEQUENCE LISTING   DATE: 02/22/2006
PATENT APPLICATION: US/10/532,014   TIME: 08:26:00

Input Set : A:\Sequence-List.txt
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```
237                  405            410              415
240 Phe Val Lys Arg Glu Ala Phe Leu Pro Phe Ser Ala Gly Arg Arg Val
241              420              425              430
244 Cys Val Gly Glu Arg Leu Ala Arg Thr Glu Leu Phe Leu Leu Phe Ala
245          435              440              445
248 Gly Leu Leu Gln Arg Tyr Arg Leu Leu Pro Pro Pro Gly Val Ser Pro
249      450              455              460
252 Ala Ser Leu Asp Thr Thr Pro Ala Arg Ala Phe Thr Met Arg Pro Arg
253 465              470              475              480
256 Ala Gln Ala Leu Cys Ala Val Pro Arg Pro
257              485              490
260 <210> SEQ ID NO: 9
261 <211> LENGTH: 2432
262 <212> TYPE: DNA
263 <213> ORGANISM: homo sapiens
265 <220> FEATURE:
266 <221> NAME/KEY: promoter
267 <222> LOCATION: (1)..(137)
268 <223> OTHER INFORMATION:
271 <220> FEATURE:
272 <221> NAME/KEY: exon
273 <222> LOCATION: (138)..(1608)
274 <223> OTHER INFORMATION:
277 <400> 9
278 gccctgcaaa ctgctcgttc cacattctcg gggtggtggg gtgggtgggg tgcgggcacg      60
280 ccctcccgcg gaggcctata agggtgcggg ggggacgggg cccaggaggg gagtggagcc     120
282 tcaccagcca cgtcctc atg gcc ctg ctg ctc ttg ctg ttc ctg ggc ctc       170
283                 Met Ala Leu Leu Leu Leu Leu Phe Leu Gly Leu
284                  1               5                  10
286 ctg ggg ctc tgg ggg ctg ctc tgc gcc tgc gcc caa gac ccc tcc cca     218
287 Leu Gly Leu Trp Gly Leu Leu Cys Ala Cys Ala Gln Asp Pro Ser Pro
288          15              20              25
290 gct gcc cgg tgg ccc ccg ggg cct cgc ccg ctg ccg ctc gtc ggg aac     266
291 Ala Ala Arg Trp Pro Pro Gly Pro Arg Pro Leu Pro Leu Val Gly Asn
292          30              35              40
294 ctg cac ttg ctg cgt ctg tcg caa cag gac cgg tcc ctg atg gag ctc     314
295 Leu His Leu Leu Arg Leu Ser Gln Gln Asp Arg Ser Leu Met Glu Leu
296      45              50              55
298 tca gaa cgc tac ggg ccg gtg ttc acc gtg cac ctg ggg cgc cag aag     362
299 Ser Glu Arg Tyr Gly Pro Val Phe Thr Val His Leu Gly Arg Gln Lys
300 60              65              70              75
302 acg gtg gtg ctg acg ggg ttc gag gcg gtc aaa gag gcg ctg gcg ggc     410
303 Thr Val Val Leu Thr Gly Phe Glu Ala Val Lys Glu Ala Leu Ala Gly
304          80              85              90
306 ccc ggg cag gag ctg gcc gac cgg cct ccc atc gcc atc ttc cag ctc     458
307 Pro Gly Gln Glu Leu Ala Asp Arg Pro Pro Ile Ala Ile Phe Gln Leu
308          95              100             105
310 atc cag cga ggt gga ggc atc ttc ttc tca tct ggg gcg cgc tgg agg     506
311 Ile Gln Arg Gly Gly Gly Ile Phe Phe Ser Ser Gly Ala Arg Trp Arg
```

W--> (marked at line 277)

```
312           110                 115                 120
314 gct gcc cgc cag ttc acg gtg cgt gcc ctg cac agc ctg ggc gtg ggc      554
315 Ala Ala Arg Gln Phe Thr Val Arg Ala Leu His Ser Leu Gly Val Gly
316           125                 130                 135
318 cgg gag ccg gtg gct gac aag att ctg cag gag ctg aaa tgc ctc tct      602
319 Arg Glu Pro Val Ala Asp Lys Ile Leu Gln Glu Leu Lys Cys Leu Ser
320 140                 145                 150                 155
322 ggg cag ctg gat ggc tac aga ggc cgg ccc ttc ccg ctg gcc cta ctg      650
323 Gly Gln Leu Asp Gly Tyr Arg Gly Arg Pro Phe Pro Leu Ala Leu Leu
324           160                 165                 170
326 ggc tgg gct ccc tcc aat atc acc ttc gcg ctc ctc ttc ggc cgc cga      698
327 Gly Trp Ala Pro Ser Asn Ile Thr Phe Ala Leu Leu Phe Gly Arg Arg
328           175                 180                 185
330 ttt gac tac cgg gac ccc gtg ttt gtg tcc ctg ctg ggt ctc atc gat      746
331 Phe Asp Tyr Arg Asp Pro Val Phe Val Ser Leu Leu Gly Leu Ile Asp
332           190                 195                 200
334 gag gtc atg gtc ctc ttg ggg tcc cct ggc ctg cag ctg ttc aac gtc      794
335 Glu Val Met Val Leu Leu Gly Ser Pro Gly Leu Gln Leu Phe Asn Val
336           205                 210                 215
338 tac cca tgg ctc ggg gcc ctg ctc cag ctg cac cgg ccc gtc ctg cgc      842
339 Tyr Pro Trp Leu Gly Ala Leu Leu Gln Leu His Arg Pro Val Leu Arg
340 220                 225                 230                 235
342 aag atc gag gag gtc cgt gcc att ctg agg acc ctc ctg gag gcg cgg      890
343 Lys Ile Glu Glu Val Arg Ala Ile Leu Arg Thr Leu Leu Glu Ala Arg
344           240                 245                 250
346 agg ccc cac gtg tgc ccg ggg gac ccc gtg tgc agc tat gtg gac gcc      938
347 Arg Pro His Val Cys Pro Gly Asp Pro Val Cys Ser Tyr Val Asp Ala
348           255                 260                 265
350 ctg atc cag cag gga cag ggg gat gac ccc gag ggc ctg ttt gct gag      986
351 Leu Ile Gln Gln Gly Gln Gly Asp Asp Pro Glu Gly Leu Phe Ala Glu
352           270                 275                 280
354 gcc aac gcg gtg gcc tgc acc ctg gac atg gtc atg gcc ggg acg gag     1034
355 Ala Asn Ala Val Ala Cys Thr Leu Asp Met Val Met Ala Gly Thr Glu
356           285                 290                 295
358 acg acc tcg gcc acg ctg cag tgg gcc gca ctt ctg atg ggc cgg cac     1082
359 Thr Thr Ser Ala Thr Leu Gln Trp Ala Ala Leu Leu Met Gly Arg His
360 300                 305                 310                 315
362 ccg gac gtg cag ggc cgg gtg cag gag gag cta gac cgc gtg ctg ggc     1130
363 Pro Asp Val Gln Gly Arg Val Gln Glu Glu Leu Asp Arg Val Leu Gly
364           320                 325                 330
366 cct ggg cgg act ccc cgg ctg gag gac cag cag gct ctg ccc tac aca     1178
367 Pro Gly Arg Thr Pro Arg Leu Glu Asp Gln Gln Ala Leu Pro Tyr Thr
368           335                 340                 345
370 agc gcc gtg ctc cac gag gtg cag cgg ttc atc acg ctc ctg ccg cac     1226
371 Ser Ala Val Leu His Glu Val Gln Arg Phe Ile Thr Leu Leu Pro His
372           350                 355                 360
374 gtg ccc cgc tgc acc gcg gcc gac aca cag ctg ggc ggc ttc ctg ctc     1274
375 Val Pro Arg Cys Thr Ala Ala Asp Thr Gln Leu Gly Gly Phe Leu Leu
376           365                 370                 375
```

VERIFICATION SUMMARY   DATE: 02/22/2006
PATENT APPLICATION: **US/10/532,014**   TIME: 08:26:01

Input Set : **A:\Sequence-List.txt**
Output Set: **N:\CRF4\02222006\J532014.raw**

```
L:12 M:270 C: Current Application Number differs, Replaced Current Application No
L:12 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:28 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:1
L:33 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:1,Line#:30
L:43 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:2
L:48 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:2,Line#:45
L:58 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:3
L:63 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:3,Line#:60
L:73 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:4
L:78 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:4,Line#:75
L:93 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:5,Line#:90
L:105 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:6
L:110 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:6,Line#:107
L:120 M:257 W: Feature value mis-spelled or invalid, <221> Name/Key for SEQ ID#:7
L:125 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:7,Line#:122
L:277 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:268
L:277 M:258 W: Mandatory Feature missing, <223> Blank for SEQ#:9,Line#:274
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